

DR WPI: 2000-687541/67.
DR N-PSDB; AAC81555.

XX
PT Growth factor homologs and the nucleic acids that encode them, useful
e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -

XX
PS Claim 1; Page 110-111; 143pp; English.

The invention relates to the human growth factor homologue zvegf4 (AAC81553), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAC81554) characterised by a PDGF cystine knot structure, and a CUB domain (AAC81555), which has a beta barrel structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3 fusions; expression constructs and host cells comprising human zvegf4 nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of hematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf4.

XX
Sequence 370 AA;
SQ

Query Match 100.0%; Score 1994; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MHLILFVYVILICANPSCSDTSATPOSASIKALRNANLRLDESHHLTLDRDETTIOWG 60
Db 1 MHLILFVYVILICANPSCSDTSATPOSASIKALRNANLRLDESHHLTLDRDETTIOWG 60

QY 61 NGYVQSPRPNPSYRNLLTWRHLHSQENTRIOLYFEDNOQGLEAENDIGRYDFEVEDIS 120
Db 61 NGYVQSPRPNPSYRNLLTWRHLHSQENTRIOLYFEDNOQGLEAENDIGRYDFEVEDIS 120

QY 121 ETSIIRIGWCGHKEVPRPIKSRTNQIKTFKSDYFVKRPGFKTYSILEDTPAASE 180
Db 121 ETSIIRIGWCGHKEVPRPIKSRTNQIKTFKSDYFVKRPGFKTYSILEDTPAASE 180

QY 181 TNWESVTSSISGVSYNSPVTDPILIAIDLKKTAEDFVDELDKYFENESWBDLENNY 240
Db 181 TNWESVTSSISGVSYNSPVTDPILIAIDLKKTAEDFVDELDKYFENESWBDLENNY 240

QY 241 LDTTRYRGSYHDKSKVLDLNDAKKYSCPTRNYSNIREEKLKANNFPRCLAQ 300
Db 241 LDTTRYRGSYHDKSKVLDLNDAKKYSCPTRNYSNIREEKLKANNFPRCLAQ 300
QY 301 RCGGNGCCTGVNWSCTCMSGKTYKHYLQFPGHKKRGRKTMALDQDHREC 360
Db 301 RCGGNGCCTGVNWSCTCMSGKTYKHYLQFPGHKKRGRKTMALDQDHREC 360
QY 361 DCICCSSRPR 370
Db 361 DCICCSSRPR 370

RESULT 2
DR AAY96864
XX ID AAY96864 standard; protein; 370 AA.

XX AC AAY96864;
XX DT 26-SEP-2000 (first entry)
XX DE SEQ. ID. 37 from WO0034474.

XX KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
KW Cysteine knot; Platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; antiarthritic;
KW vulnerable.

XX OS Homo sapiens.
XX PN WO200034474-A2.

XX PD 15-JUN-2000.

XX PR 07-DEC-1999; 99W0-US289968.

XX PR 07-DEC-1998; 98US-0207120.

XX PR 21-OCT-1999; 99US-012576.

XX PR 12-NOV-1999; 99US-0165255.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

XX PI Gilbertson DG, West JW;

XX DR WPI: 2000-423420/36.

XX DR N-PSDB; AAC81551.

XX PT Novel zvegf3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence

XX PS Disclosure; Page 164-165; 173pp; English.

Polypeptides comprising an epitope-bearing portion human or murine zvegf3 (vascular endothelial growth factor homologue) are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY81859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis toll-like protein. Structural analysis and homology predict that zvegf3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. Zvegf3 is useful for stimulating the growth of fibroblasts or smooth muscle cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. Zvegf3 is useful for regulating (post-developmental) organ growth, regeneration and maintenance, as well as tissue maintenance and repair processes. Zvegf3 antagonists are useful for treating cancer, rheumatoid arthritis, diabetic retinopathy, ischaemic limb disease, peripheral vascular disease, myocardial ischaemia, vascular intimal hyperplasia, atherosclerosis, wound healing, chronic liver disease and haemangioma formation. Zvegf3 can also be used to modulate neurite growth and development of the nervous system, and for treating neurodegenerative diseases.

XX Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 /note= "secretory peptide"
 FT 19..370
 /note= "mature protein"
 FT 52..179
 /note= "CUB domain"
 FT 180..257
 /note= "propeptide-like sequence"
 FT 258..370
 /note= "growth factor domain"
 FT
 Domain WO200151083-A1.
 PD 09-AUG-2001.
 XX
 PF 03-MAY-2000; 200000-0US12095.
 XX
 PR 04-FEB-2000; 200000-180169P.
 XX
 PR 31-MAR-2000; 200000-0540224.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PT Gilbertson DG, Hart CE;
 XX
 DR WPI; 2001-611088/70.
 DR N-PSDB; AAH4772.
 XX
 PT Use of zvegf4 polypeptide for promoting bone, ligament or cartilage growth in mammal at site of fracture, implant, and bone graft, and for promoting growth or differentiation of osteoblasts, chondrocytes in culture
 PS Example 2; Page 44-47; 57pp; English.
 XX
 CC The invention relates to the use of zvegf4 polypeptide for promoting bone, ligament or cartilage growth in a mammal, and for promoting proliferation or differentiation of osteoblasts, osteoclasts, chondrocytes or bone marrow stem cells in culture. For promoting cartilage growth, chondrocytes are cultured ex vivo in presence of the zvegf4 polypeptide and then placed into mammal where cartilage is to be grown. Zvegf4 polypeptide is useful for promoting growth of bone, ligament or cartilage in a mammal at a site of bony defect such as fracture, bone graft, implant or periodontal pocket, in humans and non-human animals such as domestic animals including livestock and companion animals. Zvegf4 is used for promoting growth of bone, ligament, or cartilage in conditions of bone defects following therapeutic treatments of bone cancers or other conditions characterized by increased bone loss or decreased bone formation, or elevation of peak bone mass in pre-menopausal woman. It is also useful for healing bone following radiation -induced osteonecrosis, repairing bone defects arising from surgery, and promotion of bone healing in plastic surgery, increasing bone formation during distraction osteogenesis, treating bone injuries including repair of cartilage and ligament and treatment of osteoporosis. The present sequence represents a human zvegf4 polypeptide.
 XX
 Sequence 370 AA;
 XX
 Query Match 100.0%; Score 1994; DB 22; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1; e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MHLILFVYTLLICANFCSCRDTSAMPOASAKLNRNRDESNHLTYRDETIVKG 60
 Db 1 MHLILFVYTLLICANFCSCRDTSAMPOASAKLNRNRDESNHLTYRDETIVKG 60
 61 NGVYQSPRFPSYPRNLLTWRHSQENTRIQVLFQGLEEAENDICRYDFVEDIS 120
 61 NGVYQSPRFPSYPRNLLTWRHSQENTRIQVLFQGLEEAENDICRYDFVEDIS 120
 OY 121 ETSTLIGRWCSEKVEPRKSRTRNQKTFKSDDFVAKPGEKIYVSLLEDFOAAPASE 180
 Db 121 ETSTLIGRWCSEKVEPRKSRTRNQKTFKSDDFVAKPGEKIYVSLLEDFOAAPASE 180
 QY 181 TNWESVTTISGSVSNNSPSVTPDTIJADALDKRAEFTWDLLYFNPESWQEDLENMY 240
 Db 181 TNWESVTTISGSVSNNSPSVTPDTIJADALDKRAEFTWDLLYFNPESWQEDLENMY 240
 QY 241 LDTPRYRGRSYHDKRSKVLDLDRNDAKRSCTPPNYSVIREELKLANVFFPCLLVQ 300
 Db 241 LDTPRYRGRSYHDKRSKVLDLDRNDAKRSCTPPNYSVIREELKLANVFFPCLLVQ 300
 QY 301 RCGGIGGGTIVNWRSCTCNGKTVKRYHEVLFEGHTIKRRGRTMAVTDQIHLHRC 360
 Db 301 RCGGIGGGTIVNWRSCTCNGKTVKRYHEVLFEGHTIKRRGRTMAVTDQIHLHRC 360
 QY 361 DCICSSRPR 370
 Db 361 DCICSSRPR 370
 RESULT 5
 AAB85529 ID AAB85529 standard; protein; 370 AA.
 XX
 AC AAB85529;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human secreted protein (clone Id HGCNC48).
 XX
 KW Secreted protein; immunosuppressive; antiarthritic; anti-rheumatic;
 KW antiproliferative; cytostatic; cardiotropic; cerebroprotective;
 KW neurotrophic; neuroprotective; antibacterial; virucide; fungicide; human;
 KW ophthalmological; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155430-A1.
 XX
 PD 02-AUG-2001.
 XX
 PR 17-JAN-2001; 2001WO-US01431.
 XX
 PR 31-JAN-2000; 200000-0179065.
 PR 04-FEB-2000; 200000-0180628.
 PR 12-SEP-2000; 200000-0231968.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
 PI Ni J, Ruben SM, Barash SC;
 XX
 DR WPI; 2001-470220/51.
 DR N-PSDB; AAH46939.
 XX
 PT 17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition
 PS Claim 11; Page 447-449; 482pp; English.
 XX
 CC The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and CC ocular disorders e.g. cornel infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent CC skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in CC chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present CC sequence represents a human secreted protein.

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MHLILFVFTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTLDRRETTIQKG 60
Qy 61 NGYVQSPRFPNSPYPRNLITWRLHSQENTRIVLFDNGGLEEAENDICRYDVEVEDIS 120
Db 61 NGYVQSPRFPNSPYPRNLITWRLHSQENTRIVLFDNGGLEEAENDICRYDVEVEDIS 120
Qy 121 EFTIITRGRWCGHKVEPRIKSRNTQNLKTFERSDDYVAKGCFKIVYSLDFQPAASE 180
121 EFTIITRGRWCGHKVEPRIKSRNTQNLKTFERSDDYVAKGCFKIVYSLDFQPAASE 180
Db 181 TWWESVTSISGVSYNSPSVDTPLADALDKKIAEFTVEDILKVNIPESWQEDLNY 240
Qy 181 TWWESVTSISGVSYNSPSVDTPLADALDKKIAEFTVEDILKVNIPESWQEDLNY 240
Db 241 LDPYRVRGRSYHDKRSVLDRLNDDAKRSYHSCIPRNSVNTREKLKLNVVFPRCLIVQ 300
Qy 301 RGGNCGCGTWNRSCTNSGKTVKHYEVLOFEPGCHIKRRGAKTMALVQDLDHERC 360
Db 301 RGGNCGCGTWNRSCTNSGKTVKHYEVLOFEPGCHIKRRGAKTMALVQDLDHERC 360
Qy 361 DCTCSSRPR 370
Db 361 DCTCSSRPR 370

XX PN W0200125437-A2.

PD 12-APR-2001.

XX PF 06-OCT-2000; 2000WO-US27671.

PF XX PR 07-OCT-1999; 99US-0158083.

PR 13-OCT-1999; 99US-0159231.

PR 04-JAN-2000; 2000US-0174485.

PR 03-MAR-2000; 2000US-0186707.

PR 10-MAR-2000; 2000US-0188250.

PR 08-AUG-2000; 2000US-0223879.

PR 12-SEP-2000; 2000US-0662783.

PR 20-SEP-2000; 2000US-0234082.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S; Jeffers M; DR WPI; 2001-316172/33.

DR N-PADB; AAS04492.

XX PT Novel growth factor polypeptides termed as FCTRX polypeptides, useful for treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders

PT XX PS Claim 1; Fig 1; 171pp; English.

CC The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as FCTRX peptides and nucleic acids. FCTRX proteins are useful for treating or preventing a disorder associated with aberrant expression, aberrant processing, or aberrant physiological interactions of the protein in a mammal, where the disorder is characterised by insufficient or ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia. The peptides and nucleic acids associated nucleic acids are useful for both promoting and inhibiting growth of cells and tissues and in treatment of cancer, anaemia, leukopenia, baldness, for treating cardiovascular and fibrotic disorders, diabetic ulcers, obesity, infectious diseases, hyperproliferative and dysproliferative disorders, neurodegenerative disorders, osteoarthritis, inflammatory disorders, graft versus host disease, coagulation disorders such as haemophilia, and neural disorders including Parkinson's disease, Alzheimer's disease, multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury and epilepsy.

CC SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MHLILFVFTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTLDRRETTIQKG 60
Qy 61 NGYVQSPRFPNSPYPRNLITWRLHSQENTRIVLFDNGGLEEAENDICRYDVEVEDIS 120
Db 61 NGYVQSPRFPNSPYPRNLITWRLHSQENTRIVLFDNGGLEEAENDICRYDVEVEDIS 120

XX OS Homo sapiens.

XX Key Location/qualifiers 1..23
FT Peptide /note= "Signal peptide"
FT Protein /note= "Mature FCTRL"
FT Domain 53..167

QY	121	ESTSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDYFVAKPGFKIYKISLLEDQPAASE	180	CC
Db	121	ESTSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDYFVAKPGFKIYKISLLEDQPAASE	180	CC
Db	181	TNWESVTSSISGVSYNSPVTDPITLADAKKIAEFTDVEDLILYFNPESQEDMLNY	240	CC
QY	181	TNWESVTSSISGVSYNSPVTDPITLADAKKIAEFTDVEDLILYFNPESQEDMLNY	240	CC
Db	241	LDTPRYRGSRSYHDKSKVLDLDRNDAKRSCTPPNSYNTREELKLANTVFPCLLQ	300	CC
Db	241	LDTPRYRGSRSYHDKSKVLDLDRNDAKRSCTPPNSYNTREELKLANTVFPCLLQ	300	CC
QY	301	RCGGNCGGTIVNWRSCTCNSGKTVKYHEVLOFEPGHIKRGRAKTMAVLVDIQLDHERC	360	CC
Db	301	RCGGNCGGTIVNWRSCTCNSGKTVKYHEVLOFEPGHIKRGRAKTMAVLVDIQLDHERC	360	CC
QY	361	DCICSSRPR 370	361	CC
Db	361	DCICSSRPR 370	361	CC
RESULT 7				
AAU00704	ID	AAU00704 standard; Protein; 370 AA.		
XX	AC	AAU00704;		
XX	DT	07-SEP-2001 (first entry)		
XX	DE	Human PDGF protein.		
XX	KW	Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor; VEGF-E; platelet derived growth factor; PDGF; FGF; hyperplasia; cancer; neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder; fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human; dysproliferation; neurodegenerative disorder; osteoarthritis; inflammatory disorder; Graft versus host disease; coagulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis; peripheral neuropathy; acute brain injury.		
XX	OS	Homo sapiens.		
XX	PN	WO200125437-A2.		
XX	PD	12-APR-2001.		
XX	PF	06-OCT-2000; 2000WO-US27671.		
XX	PR	07-OCT-1999; 99US-0158083.		
PR	PR	13-OCT-1999; 99US-0159231.		
PR	PR	04-JAN-2000; 2000US-0174485.		
PR	PR	03-MAR-2000; 2000US-0186707.		
PR	PR	10-MAR-2000; 2000US-0188250.		
PR	PR	08-AUG-2000; 2000US-0223879.		
PR	PR	12-SEP-2000; 2000US-0662783.		
XX	XX	20-SEP-2000; 2000US-0234082.		
(CURA') CURAGEN CORP.				
XX	PI	Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S; PI Jeffers M;		
XX	DR	WPI; 2001-316172/33.		
XX	N-PSDB	AAS04498.		
PT	PT	Novel growth factor polypeptides termed as FCTRX polypeptides, useful for treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders		
XX	PS	Disclosure; Fig 13; 171PP; English.		
XX	The sequence represents a protein related to bone morphogenetic protein-1			
RESULT 8				
AAE00999	ID	AAE00999 standard; Protein; 370 AA.		
XX	AC	AAE00999;		
XX	DT	04-JUL-2001 (first entry)		
XX	DE	Human Zvegf4 protein which forms heteromultimer with Zvegf3 protein.		
XX	KW	Human; Zvegf3 antagonist; cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; PDGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosi; diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis; asbestos; renal arteriosclerosis; post necrotic cirrhosis; diabetic glomerulosclerosis; focal glomerulosclerosis; pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;		

KW	bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;	Db	241	LDMPRYRGRSYHDKSKVDDLRNDDAKRYSCPTPRNYSVNTEELKANVVFPRCLLVQ
XX	fibroproliferative disorder; zvegf4 protein.	Qy	301	RCGGNCGGTVWRSCTCNSGKTVKKHEVLOFEPGHIKRGRAKTMALVQDQDHHRC
OS	Homo sapiens.	Db	301	RCGGNCGGTVWRSCTCNSGKTVKKHEVLOFEPGHIKRGRAKTMALVQDQDHHRC 360
XX				
PN	WO200128586-A1.			
XX				
PD	26-APR-2001.			
XX				
PF	23-OCT-2000; 2000WO-US29270.			
XX				
PR	21-OCT-1999; 99US-0161653.			
PR	12-NOV-1999; 99US-0165255.			
PR	01-AUG-2000; 2000US-0222223.			
XX				
PA	(ZYMO) ZYMOGENETICS INC.			
XX				
PI	Gilbertson DG;			
XX				
DR	WPI; 2001-300278/31.			
XX				
PT	Use of zvegf3 antagonist for reducing fibroproliferative disorder of kidney, liver and bone, reducing extracellular matrix production, treating fibrosis or reducing stellate cell activation in mammal			
XX				
PS	Disclosure; Page 62-63; 70pp; English.			
XX				
CC	The patent discloses materials and methods for reducing cell proliferation or extracellular matrix production, treating fibrosis and reducing stellate cell activation in a mammal. The method comprises administering a composition containing a zvegf3 antagonist in combination with a delivery vehicle. The zvegf3 is a protein that is structurally related to platelet-derived growth factor (pdgf) and the vascular endothelial growth factors (VEGF). The zvegf3 protein is also designated as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat keloids, scleroderma, fibrotic disorders of liver such as chronic active hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders of the lung such as silicosis, asbestos, idiopathic pulmonary fibrosis, bronchiolitis obliterans organising pneumonia and pulmonary hypertension, fibrotic disorders of pancreas, fibroproliferative disorders of the vasculature such as transplant vasculopathy and fibroproliferative disorders of the bone such as osteopetrosis and hyperostosis. The present sequence is human zvegf4 protein which forms a heteromultimer with zvegf3 protein.			
XX				
Sequence	370 AA;			
Query Match	100.0%; Score 1994; DB 22; Length 370;			
Best Local Similarity	100.0%; Pred. No. 1; 1e-188;			
Matches	370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 MHLILFVYTLCIANFCSCRTDATPOSASIKALRNANLRDESNHLTDLYRDETIQKG 60			
Db	1 MHLILFVYTLCIANFCSCRTDATPOSASIKALRNANLRDESNHLTDLYRDETIQKG 60			
Qy	61 NGVQSPRSPNPSPRNLLTWRHLSQENTRIQLVFDQGLEAENDICRYDEVEDIS 120			
Db	61 NGVQSPRSPNPSPRNLLTWRHLSQENTRIQLVFDQGLEAENDICRYDEVEDIS 120			
Qy	121 EFTIIRRGWCGKEVPRKSRINQKTFKNSDDYVAKPGFKIYSSLLEDQPAASE 180			
Db	121 EFTIIRRGWCGKEVPRKSRINQKTFKNSDDYVAKPGFKIYSSLLEDQPAASE 180			
Qy	181 TNWESVTISIGSYNSNSVPTLIAADKKIAETDVEILKYPNPEQDLEN 240			
Db	181 TNWESVTISIGSYNSNSVPTLIAADKKIAETDVEILKYPNPEQDLEN 240			
Qy	241 LDPPRYSRHYRSKLDRNDARYSCPRNYSNIRELKANVWPRCLVQ 300			
Sequence	370 AA;			
Query Match	100.0%; Score 1994; DB 22; Length 370;			
Best Local Similarity	100.0%; Pred. No. 1; 1e-188;			
Matches	370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 MHLILFVYTLCIANFCSCRTDATPOSASIKALRNANLRDESNHLTDLYRDETIQKG 60			
Db	1 MHLILFVYTLCIANFCSCRTDATPOSASIKALRNANLRDESNHLTDLYRDETIQKG 60			
Qy	61 NGVQSPRSPNPSPRNLLTWRHLSQENTRIQLVFDQGLEAENDICRYDEVEDIS 120			

61	NGYVOSPREFNSPYRNLLTWRQSQENTRQLVDNQGLEAENDTCYDFEVEDIS	120
QY		CC
121	ETSTIRGRMGHKEVPPRKSRTNQIKITFKSDDFYVAKPGFKIYSLLEDFOQAASE	180
Db	ETSTIRGRMGHKEVPPRKSRTNQIKITFKSDDFYVAKPGFKIYSLLEDFOQAASE	180
181	TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240
181	TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240
QY		CC
181	TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240
Db	181 TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240
241	LDTPRGRGSHDRSKVLDLNDAKRYSCTPRNSYNTREELKLANTVFPCLLQ	300
QY		CC
241	LDTPRGRGSHDRSKVLDLNDAKRYSCTPRNSYNTREELKLANTVFPCLLQ	300
Db	241 LDTPRGRGSHDRSKVLDLNDAKRYSCTPRNSYNTREELKLANTVFPCLLQ	300
361	DCICSSRPPR 370	360
QY		CC
361	DCICSSRPPR 370	360
Db	361 DCICSSRPPR 370	360
RESULT 10		
ABP51640		
ID		
ABP51640 standard; Protein; 370 AA..		
XX		
AC		
AC ABP51640;		
XX		
DR		
30-SEP-2002 (first entry)		
XX		
DE		
Human zvegf4 protein SEQ ID NO:2.		
XX		
KW		
Human; zvegf4; cell proliferation; extracellular matrix production; fibroproliferative disorder; PDGF-D; platelet derived growth factor; PDGF; vascular endothelial growth factor; VEGF; cytostatic; nephrotoxic; hepatotropic; antiinflammatory; osteopathic; antiarrhythmic; metastasis; prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis; diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome; chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis; hyperostosis; osteoarthritis; Homo sapiens.		
XX		
PN		
US2002064832-A1.		
XX		
PD		
30-MAY-2002.		
XX		
PF		
14-MAR-2001; 2001US-0808972.		
XX		
PR		
03-MAY-1999; 99US-132250P.		
PR		
10-NOV-1999; 99US-164463P.		
PR		
04-FEB-2000; 2000US-180169P.		
PR		
26-SEP-2000; 2000US-235299P.		
PR		
03-MAY-2000; 2000US-0564995.		
XX		
PA		
(HART /) HART C E.		
PA		
(TOPOL) TOPOULIS S.		
PA		
(GILB /) GILBERTSON D G.		
XX		
PI		
Hart CE, Topouzis S, Gilbertson DG;		
XX		
DR		
WPI; 2002-573696/61.		
XX		
N-PSDB; ABQ73239.		
PT		
Reducing proliferation or extracellular matrix production by a cell in		
PT		
a mammal, useful for treating fibroproliferative disorders of bone, liver and kidney, comprises administering a zvegf4 antagonist		
XX		
Example 3; Page 19-20; 34pp; English.		
XX		
The present invention describes a method for reducing proliferation of		
CC		
or extracellular matrix production by a cell in a mammal. The method comprises administering to the mammal a composition comprising a therapeutically effective amount of a zvegf4 antagonist chosen from anti-zvegf4 antibodies, inhibitory polynucleotides, inhibitors of zvegf4 activation, and mitogenically inactive, receptor-binding variants of zvegf4. Zvegf4 (also called PDGF-D) is a multi-domain protein that is structurally related to platelet derived growth factor (PDGF) and vascular endothelial growth factors (VEGF). Zvegf4 has cytostatic, nephrotoxic, hepatotropic, antiinflammatory, osteopathic and antiarthritic activities. The method is useful for reducing proliferation of mesangial, epithelial, endothelial, smooth muscle, fibroblast, osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells in a mammal, in particular proliferation of prostate tumour cells, and for reducing extracellular matrix production by a cell in a mammal suffering from a fibroproliferative disorder of kidney, bone or liver. In particular it is useful for reducing stellate cell activation. The method is useful for reducing metastasis of prostate cancer cells to bone in a mammal and for treating a fibroproliferative disorder of kidney, liver or bone in a mammal. Fibroproliferative disorders of the kidney, liver or bone in a mammal, diabetic glomerulosclerosis, lupus nephritis, renal arteriosclerosis and nephrotic syndrome, disorders of the liver include chronic active hepatitis and many other types of cirrhosis, and disorders of the bone include osteopetrosis, osteosclerosis, osteoarthritis, and ectopic bone formation in metastatic prostate cancer. The present sequence represents human zvegf4, which is used in an example from the present invention.		
XX		
SQ		
Sequence 370 AA:		
Query Match 100.0%; Score 1994; DB 23; Length 370;		
Best Local Similarity 100.0%; Pred. No. 1.1e-188;		
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY		
1 MHLRLFVYTTCANFCSRCDSATPOSASTKALRNALRDESNHJTLYRDETQKG	60	CC
1 MHLRLFVYTTCANFCSRCDSATPOSASTKALRNALRDESNHJTLYRDETQKG	60	CC
QY		
61 NGYVOSPREFNSPYRNLLTWRQSQENTRQLVDNQGLEAENDICRDFVVEDIS	120	CC
61 NGYVOSPREFNSPYRNLLTWRQSQENTRQLVDNQGLEAENDICRDFVVEDIS	120	CC
Db		
121 ETSTIRGRMGHKEVPPRKSRTNQIKITFKSDDFYVAKPGFKIYSLLEDFOQAASE	180	CC
121 ETSTIRGRMGHKEVPPRKSRTNQIKITFKSDDFYVAKPGFKIYSLLEDFOQAASE	180	CC
Db		
181 TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240	CC
181 TNWEVTSSISGVSYNSPSTDPTLJADLKKAEFDVTDLLKYNPESQWQDLENMY	240	CC
QY		
241 LDTPRGRGSHDRSKVLDLNDAKRYSCTPRNSYNTREELKLANTVFPCLLQ	300	CC
241 LDTPRGRGSHDRSKVLDLNDAKRYSCTPRNSYNTREELKLANTVFPCLLQ	300	CC
Db		
301 RCGGNCGCGTWNRSCTCNSGKTVKHYEVLQFEGHKGKRGAKTMAVLQDQDHRC	360	CC
301 RCGGNCGCGTWNRSCTCNSGKTVKHYEVLQFEGHKGKRGAKTMAVLQDQDHRC	360	CC
Db		
361 DCTCSSRPPR 370	360	CC
Db		
361 DCTCSSRPPR 370	360	CC
RESULT 11		
ABG64733		
ID		
ABG64733 standard; Protein; 370 AA.		
XX		
AC		
ABG64733;		
XX		
27-AUG-2002 (first entry)		
XX		
DE		
Human albumin fusion protein #1408.		
XX		
KW		
Albumin fusion protein; therapeutic protein X; human albumin; HA;		

kw human serum albumin; HSA; cancer; reproductive disorder;
 kw digestive disorder; immune disorder; endocrine disorder;
 kw haemopoietic disorder; neural disorder; connective disorder;
 kw cytostatic; antinifertility; antiinflammatory; antiulcer;
 kw immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
 kw neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 kw osteopathic; antiarthritic.
 xx
 os Homo sapiens.
 os Synthetic.
 xx
 PN WO200177137-A1.
 xx
 PD 18-OCT-2001.
 xx
 PR 12-APR-2001; 2001WO-US11988.
 xx
 PR 12-APR-2000; 2000US-129358P.
 PR 25-APR-2000; 2000US-199384P.
 PR 21-DEC-2000; 2000US-256931P.
 xx
 PA (HUMA-) HUMAN GENOME SCI INC.
 xx
 PR Rosen CA, Hasettine WA;
 xx
 DR WPI; 2002-010886/01.
 xx
 PR New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -
 xx
 FS Claim 1; Page 1459-1460; 2102PP; English.
 xx
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS, endocrine disorders
 CC (e.g. diabetes), haemopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG3326-ABG65518 represent albumin
 xx
 SQ Sequence 370 AA:
 Query Match 100.0%; Score 1994; DB 23; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1, 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 MHLIFIVTTLICANFCSDRTSATPOASIKALRNANLRRDESNHLDLYRDETOVKG 60
 DB 1 MHLIFIVTTLICANFCSDRTSATPOASIKALRNANLRRDESNHLDLYRDETOVKG 60
 QV 61 NGVQSPREPNSPRLNLTWRLHSQENTRQLVFDQFNGLEAENDICRYPVEEDIS 120
 DB 61 NGVQSPREPNSPRLNLTWRLHSQENTRQLVFDQFNGLEAENDICRYPVEEDIS 120
 QV 181 TNNEVSISISGVSYNSNSVTDPFLIAALDKKIAEPTVEDILKYPNPEQEDLNEY 240
 DB 181 TNNEVSISISGVSYNSNSVTDPFLIAALDKKIAEPTVEDILKYPNPEQEDLNEY 240
 QV 241 LDTPRVRYSRHSKDKLDRNDARRYSCPRNTSVNIREKLKLNVWRPCLVQ 300
 DB 241 LDTPRVRYSRHSKDKLDRNDARRYSCPRNTSVNIREKLKLNVWRPCLVQ 300
 SQ Sequence 370 AA:
 Query Match 100.0%; Score 1994; DB 23; Length 370;
 QY 301 RCGGNCGGTVWNRCTONSGKTVKKHEVQFEPGKIKRRGRAKTMLVDIQLDHERC 360
 DB 301 RCGGNCGGTVWNRCTONSGKTVKKHEVQFEPGKIKRRGRAKTMLVDIQLDHERC 360
 QY 361 DCICSSRPR 370
 DB 361 DCICSSRPR 370
 RESULT 12
 AAB47891
 ID AAB47891 standard; Protein; 370 AA.
 XX
 AC AAB47891;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human zvegf4.
 XX
 PR Human; mouse; zvegf3; zvegf4; platelet derived growth factor;
 KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;
 KW osteoblast; chondrocyte; bony defect; fracture; bone graft;
 KW implant; periodontal pocket; osteoclast; bone marrow stem cell;
 KW Osteoporosis.
 XX
 OS Homo sapiens.
 XX
 PN US2002004225-A1.
 PD 10-JAN-2002.
 XX
 PF 29-MAR-2001; 2001US-0823033.
 XX
 PR 07-DEC-1998; 9805-111173P.
 PR 06-JUL-1999; 9905-142576P.
 PR 21-OCT-1999; 9905-161653P.
 PR 12-NOV-1999; 9905-165255P.
 PR 31-MAR-2000; 2000US-193723P.
 PR 07-DEC-1999; 9905-0457066.
 XX
 PA (HART/) HART C E.
 PA (GILB/) GILBERTSON D G.
 XX
 PT Hart CE, Gilbertson DC;
 XX
 DR WPI; 2002-171026/22.
 XX
 PT Promoting growth of bone, ligament or cartilage in a mammal, involves
 PT administering to the mammal a protein which comprises growth factor
 PT domain of zvegf3 protein, a homolog of platelet-derived growth factor
 PT
 PS Claim 8; Page 20-21; 31PP; English.
 XX
 CC This sequences represents human zvegf4. zvegf4 can be used in a
 CC composition with either human or mouse zvegf3, for promoting growth of
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
 CC or chondrocytes in a mammal. zvegf3 is a platelet derived growth factor
 CC (PDGF) homolog. The zvegf3 protein used was preferably a dimeric
 CC protein of residues 235 of human zvegf3 or all of the mouse zvegf3
 CC protein, with a delivery vehicle. The method of th invention is useful
 CC for promoting growth of bone, ligament or cartilage in a mammal, where
 CC the composition is administered at a site of a bony defect, preferably
 CC a fracture, bone graft site, implant site, or periodontal pocket, and
 CC for stimulating proliferation of osteoblasts or chondrocytes in a
 CC mammal. It is further useful for promoting proliferation of osteoblasts,
 CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis.
 XX
 Sequence 370 AA:
 Query Match 100.0%; Score 1994; DB 23; Length 370;

Best Local Similarity	100.0%	Pred.	No.	1.e-18;	DR	N-PSDB; AAD15819.			
Matches	370;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	PS	XX	PT	Analog of a platelet-derived growth factor homolog, LP85 useful for		
Db	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	PT	XX	PT	treating osteoporosis, arthritis, sarcopenia, wounds, has one or more		
QY	61	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	PR	XX	PR	amino acid substitutions which destroy the tripeptidyl sequence of		
Db	121	ETSTIRGRWGHKEPPRKSRTNQIKITKSDDFVAKGFKIYSLLEDFOPARASE	180	PT	XX	PT	native LP85 -		
QY	181	TNWESYTSSISGVSYNSPSVDTPLTADALDKKIAEFTDVEDLKYFNPESWQEDLENMY	240	CC	XX	PS	Claim 11; Page 109-110; 117pp; English.		
Db	181	TNWESYTSSISGVSYNSPSVDTPLTADALDKKIAEFTDVEDLKYFNPESWQEDLENMY	240	CC	XX	XX	The present invention relates to LP85, an analogue of platelet-derived		
QY	241	LDTPRYRGSRSHDRSKVUDLRLNDAAKRYSCTPRNIVSNVREELKLANVVFPRLVQ	300	CC	XX	CC	growth factor (PDGF) homologue. Sequences of the invention are useful		
Db	241	LDTPRYRGSRSHDRSKVUDLRLNDAAKRYSCTPRNIVSNVREELKLANVVFPRLVQ	300	CC	XX	CC	for the manufacture of a medicament for treating musculoskeletal disorder		
QY	301	RGGNGGCGTGNWRSCCTNSKTVKHYEVLOFEPCHIKRGRAKMALVIDIQLHRC	360	CC	XX	CC	(MSD) which include promoting bone growth, cartilage differentiation and		
Db	301	RGGNGGCGTGNWRSCCTNSKTVKHYEVLOFEPCHIKRGRAKMALVIDIQLHRC	360	CC	XX	CC	function, wound healing, neuron growth, preventing cartilage degradation		
QY	361	DCICSSRPPR	370	CC	XX	CC	or neuronal degeneration. They are useful for treating bone fractures,		
Db	361	DCICSSRPPR	370	CC	XX	CC	osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,		
QY	370			CC	XX	CC	tissue atrophy, traumatised connective tissues, grafted connective		
Db	370			CC	XX	CC	tissues and/or transplanted organs, bone or muscle loss due to		
QY	370			CC	XX	CC	malignancy, endocrine disorders and immobility. They are also used		
Db	370			CC	XX	CC	prophylactically increasing or maintaining bone density in a		
QY	370			CC	XX	CC	mammal. The present sequence is human LP85 protein.		
Db	370			CC	XX	CC	Sequence 370 AA;		
QY	370			CC	XX	CC	Query Match 100.0%; Score 1994; DB 23; Length 370;		
Db	370			CC	XX	CC	Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	Db	1	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
Db	61	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	QY	61	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	61	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	181	TNWESYTSSISGVSYNSPSVDTPLTADALDKKIAEFTDVEDLKYFNPESWQEDLENMY	240	QY	181	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	181	TNWESYTSSISGVSYNSPSVDTPLTADALDKKIAEFTDVEDLKYFNPESWQEDLENMY	240	Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	241	LDTPRYRGSRSHDRSKVUDLRLNDAAKRYSCTPRNIVSNVREELKLANVVFPRLVQ	300	QY	241	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	241	LDTPRYRGSRSHDRSKVUDLRLNDAAKRYSCTPRNIVSNVREELKLANVVFPRLVQ	300	Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	301	RGGNGGCGTGNWRSCCTNSKTVKHYEVLOFEPCHIKRGRAKMALVIDIQLHRC	360	QY	301	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	301	RGGNGGCGTGNWRSCCTNSKTVKHYEVLOFEPCHIKRGRAKMALVIDIQLHRC	360	Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	361	DCICSSRPPR	370	QY	361	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	361	DCICSSRPPR	370	Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	121	1	MHLIFIVYTLLICANFCSCRDTSATPOSASIKRALRNALRDRDESNHLTDLYRDETQVKG	60	
QY	370			QY	370	1	NGYVOSPRFPNSYPRNLLTWRHSOENTRQLVFDNQGLEAENDICRYDFVEEDIS	120	
Db	370			Db	12				

XX	OS	Homo sapiens.
XX	OS	Synthetic.
FH	Key	Location/Qualifiers
FT	Misc-difference	275 /note= "Wild type Asn substituted with Asp"
FT	W0200189450-A2.	
PN		
XX		
PD	29-NOV-2001.	
XX		
PF	08-MAY-2001; 2001WO-US11755.	
XX		
PR	19-MAY-2000; 2000US-205124P.	
PR	11-JAN-2001; 2001US-261071P.	
PR	11-JAN-2001; 2001US-261076P.	
PR		
PA	(ELIL) LILLY & CO ELI.	
XX		
PI	Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;	
PI	Witcher DR, Wroblewski VJ;	
XX		
WPI:	2002-083040/11.	
XX		
PT	Analog of a platelet-derived growth factor homolog, LP85 useful for treating osteoporosis, arthritis, sarcopenia, wounds, has one or more amino acid substitutions which destroy the tripeptidyl sequence of native LP85 -	
PT		
XX		
PS	Claim 15b; Page -; 117pp; English.	
XX		
CC	The present invention relates to LP85, an analogue of Platelet-derived growth factor (PDGF) homologue. Sequences of the invention are useful for the manufacture of a medicament for treating musculoskeletal disorder (MSD) which include promoting bone growth, cartilage differentiation and function, wound healing, neuron growth, preventing cartilage degradation or neuronal degeneration. They are useful for treating bone fractures, osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease, tissue atrophy, traumatised connective tissues, grafted connective tissues and/or transplanted organs, bone or muscle loss due to malignancy, endocrine disorders and immobility. They are also used for prophylactically increasing or maintaining bone density in a mammal. The present sequence is human LP85 mutant protein (N276D).	
CC	Note: This sequence is not shown in the specification but is derived from human LP85 protein shown in pages 109-110 of the specification (AAE15819).	
CC		
XX		
SQ	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
SQ	Query Match	99.7%; Score 1989; DB 23; Length 370;
XX	Best Local Similarity	99.7%; Pred. No. 3.5e-188;
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
QY	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
Db	61 NGYVQSPRFPSVPRNLLWRLHSQENTRQLVDPNQFGLAEENDICRYDFVEEDIS 120	
QY	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
Db	121 EMTITRGRCGHKEVPPRKSRTNQIKITPKSDDFVVKPGFKIYSSLEDFQPAASE 180	
QY	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
Db	181 TNWESVTSTSGVSYNSPSVYDPTLIAADKKLAEFDVTDLKVFPSPSQELEMNY 240	
QY	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
Db	241 LDTPRVRGRSRYHDKSKVLDLRLNDAAKRYSCTPRIVSNIREELKLNVVFFPRLVQ 300	
XX		
PS	Sequence 370 AA;	
XX		
Query Match	99.7%; Score 1989; DB 23; Length 370;	
Best Local Similarity	99.7%; Pred. No. 3.5e-188;	
Matches	369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MHLIFVYTLLCANPSCSRISATPOSASIKALRNRLRDESNHILTYRDETQWKG 60	
Db	1 MHLIFVYTLLCANPSCRDISATPOSASIKALRNRLRDESNHILTYRDETQ	

XX
Sequence 370 AA:

Query Match 99.7%; Score 1989; DB 23; Length 370;
Best Local Similarity 99.7%; Pred. No. 3; Se. 188;
Matches 369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHLIFVTLICANFCSCRDTSATPOQASIKALRNANLRRDESNHLTLDRRDETIQKG 60
Db 1 MHLIFVTLICANFCSCRDTSATPOQASIKALRNANLRRDESNHLTLDRRDETIQKG 60
Qy 61 NGVQSPREPNSPRLNLTWRLHSQENTR10LVEDNOFGLEAENDICRYFVEEDIS 120
Db 61 NGVQSPREPNSPRLNLTWRLHSQENTR10LVEDNOFGLEAENDICRYFVEEDIS 120
Qy 121 ESTIITRGWRWCGHKEVPRIKSRNTQIKITFSDDYWAKPGKIVYSLLEDQPAASE 180
Db 121 ESTIITRGWRWCGHKEVPRIKSRNTQIKITFSDDYWAKPGKIVYSLLEDQPAASE 180
Qy 181 TNWESVTSISCGSYNSFSVNDPTLADALDKKIAEFDVEDLKYFNPESQEDLNY 240
Db 181 TNWESVTSISCGSYNSFSVNDPTLADALDKKIAEFDVEDLKYFNPESQEDLNY 240
Qy 241 LDTPRYRGRSYHDKSKVLDRLNDKRYSTPRNYSNTREELKIANVFFPCLVQ 300
Db 241 LDTPRYRGRSYHDKSKVLDRLNDKRYSTPRNYSNTREELKIANVFFPCLVQ 300
Qy 301 RCGGNGCGGTWNRSCCTCNSGKTVKKHHEVLOFEPGHKRGRAKTMALVTDOLDHHERC 360
Db 301 RCGGNGCGGTWNRSCCTCNSGKTVKKHHEVLOFEPGHKRGRAKTMALVTDOLDHHERC 360
Qy 361 DCICSSRPR 370
Db 361 DCICSSRPR 370

Search completed: June 12, 2003, 15:29:58
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 12, 2003, 15:28:35 ; Search time 26 Seconds
(without alignments)
418.711 Million cell updates/sec

Title: US-09-662-783-2
Perfect score: 1994
Sequence: 1 MHRLLFVYTLICANFCSCRD.....DIQLDHHERCDCICSSRPPR 370
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/7A_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/7B_COMB.pep: *

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1994	100.0	370	4	US-09-457-066-37
2	1994	100.0	370	4	US-09-540-224-2
3	1737	87.1	370	4	US-09-540-224-4
4	752	37.5	345	4	US-09-457-066-4
5	742.5	37.2	345	4	US-09-040-220D-2
6	742.5	37.2	345	4	US-09-457-066-2
7	742.5	37.2	345	4	US-09-265-686-2
8	742.5	37.2	345	4	US-09-540-224-5
9	187.5	9.4	788	1	US-08-572-225-1
10	180.5	9.4	730	4	US-08-872-757-2
11	180.5	9.1	101	4	US-09-374-135-6
12	174.5	8.8	986	4	US-08-872-757-4
13	172.5	8.7	591	3	US-08-991-408-4
14	172.5	8.7	591	4	US-09-432-473-4
15	172.5	8.7	1013	2	US-08-866-650-5
16	172.5	8.7	1013	2	US-09-287-5
17	172.5	8.7	1013	3	US-08-991-408-2
18	172.5	8.7	1013	4	US-09-240-473-5
19	172.5	8.7	1013	4	US-09-432-473-2
20	167.5	8.4	103	4	US-09-135-5
21	167	8.4	922	4	US-09-116-473-4
22	166.5	8.4	1013	2	US-08-866-650-3
23	166.5	8.4	1013	2	US-09-021-877-3
24	166.5	8.4	1013	4	US-09-240-473-3
25	164	8.2	923	3	US-08-935-135-6
26	159	8.0	909	3	US-08-935-135-18
27	8.0	926	3	US-08-936-135-20	

ALIGNMENTS

RESULT 1:
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Christopher E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVECF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PR
; ORGANISM: Homo sapiens
; US-09-457-066-37

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.7e-198;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDMSATQASASTKALRNRLRDESNNLTDLYRDRDTQVKG 60
1 MHRLLFVYTLICANFCSCRDMSATQASASTKALRNRLRDESNNLTDLYRDRDTQVKG 60

Db 61 NGYVQSPREPNSYPRMLLTLWHLQENTRQLQVFDNQFGLAEANDICRYDFEVEDIS 120
61 NGYVQSPREPNSYPRMLLTLWHLQENTRQLQVFDNQFGLAEANDICRYDFEVEDIS 120

QY 121 ETSTLIRGRMGKHEVKPRRSRTQKIKITFKSDDFVAKPGFKIYSLIEDFQRAASE 180
121 ETSTLIRGRMGKHEVKPRRSRTQKIKITFKSDDFVAKPGFKIYSLIEDFQRAASE 180

Db 121 ETSTLIRGRMGKHEVKPRRSRTQKIKITFKSDDFVAKPGFKIYSLIEDFQRAASE 180
121 ETSTLIRGRMGKHEVKPRRSRTQKIKITFKSDDFVAKPGFKIYSLIEDFQRAASE 180

QY 181 TNWESTTSISGSVNSNSPVSYDPTLJADLKKIEFDFTWDLIYFNPNSWQEDLENMY 240
181 TNWESTTSISGSVNSNSPVSYDPTLJADLKKIEFDFTWDLIYFNPNSWQEDLENMY 240

Db 181 TNWESTTSISGSVNSNSPVSYDPTLJADLKKIEFDFTWDLIYFNPNSWQEDLENMY 240
181 TNWESTTSISGSVNSNSPVSYDPTLJADLKKIEFDFTWDLIYFNPNSWQEDLENMY 240

QY 241 LDTPRYRGSRSHDRSKVUDLDRNDAKRSCTPRMYSWIREEKLANYVFPCLLQ 300
241 LDTPRYRGSRSHDRSKVUDLDRNDAKRSCTPRMYSWIREEKLANYVFPCLLQ 300

QY 301 RCGGNGCGTIVNWRSCCNCSKTVKHYHEVQFEGHIIKRRGAKTMAVLVDIQLDHERC 360
301 RCGGNGCGTIVNWRSCCNCSKTVKHYHEVQFEGHIIKRRGAKTMAVLVDIQLDHERC 360

RESULT 2
 US 09-540-224-2
 ; Sequence 2, Application US/09540224
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbertson, Debra G.
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
 ; FILE REFERENCE: 00-28
 ; CURRENT APPLICATION NUMBER: US/09/540, 224
 ; CURRENT FILING DATE: 2000-03-31
 ; EARLIER FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-540-224-2

Query Match 87.1%; Score 1737; DB 4; Length 370;
 Best Local Similarity 85.1%; Pred. No. 2e-171; Mismatches 315; Conservative 25; Indels 0; Gaps 0;
 Matches 315; Mismatches 30; Indels 0; Gaps 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLLICANFCSCDTSATPOSASIKALRNANLRDESHLTDIYRDETIQVG 60
 Db 1 MHRLLFVYTLLICANFCSCDTSATPOSASIKALRNANLRDESHLTDIYRDETIQVG 60

Qy 61 NGYVQSPREPNSPYRNLLTWRJLQSENTRIQLYFDNQGLEEENDICRYDFEVEDIS 120
 Db 61 NGYVQSPREPNSPYRNLLTWRJLQSENTRIQLYFDNQGLEEENDICRYDFEVEVIS 120

Qy 121 ETSTTIRGRMGKHKVTPRSTSRTNQIKTFKSDDFYVAKPGFKIYSSILEDQPAASE 180
 Db 121 ESTTIRGRMGKHKVTPRSTSRTNQIKTFKSDDFYVAKPGFKIYSSILEDQPAASE 180

Qy 181 TNWESVTSSISGVNSNSPVDPTIADALDKKIAEFDVEDILKYYENESWORLDENNY 240
 Db 181 TNWESVTSSISGVNSNSPVDPTIADALDKKIAEFDVEDILKYYENESWORLDENNY 240

Qy 241 LDTPRYRGSRSYHDKSKVDPDLRNDAKRYSCTPRNYSVNIREFKLANVFPRLCLVQ 300
 Db 241 LDTPRYRGSRSYHDKSKVDPDLRNDAKRYSCTPRNYSVNIREFKLANVFPRLCLVQ 300

Qy 301 RCGGNCGCTVNRSCCTCNSGKTVKHYEVILQFEGHKKRGRAKTMAVLVIDQLDHERC 360
 Db 301 RCGGNCGCTVNRSCCTCNSGKTVKHYEVILQFEGHKKRGRAKTMAVLVIDQLDHERC 360

Qy 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370

RESULT 3
 US-09-540-224-4
 ; Sequence 3, Application US/09540224
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, Charles E.
 ; PATENT NO. 6468543
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
 ; FILE REFERENCE: 00-28
 ; CURRENT APPLICATION NUMBER: US/09/540, 224

RESULT 4
 US-09-457-066-43
 ; Sequence 4, Application US/09457066
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Shoemaker, Kimberly E.
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: West, James W.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
 ; FILE REFERENCE: 98-60
 ; CURRENT APPLICATION NUMBER: US/09/457, 066
 ; CURRENT FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 43
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-457-066-43

Query Match 37.7%; Score 752; DB 4; Length 345;
 Best Local Similarity 45.3%; Pred. No. 1.8e-69;
 Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

Qy 42 ESNHLDIYRDETIQVGNGVQSPREPNSPYRNLLTWRJLQSENTRIQLYFDNQFG 100

RESULT 5
 US-09-040-220D-2
 ; Sequence 2, Application US/09040220D
 ; Patent No. 6391311
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
 ; ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
 ; PROTEIN 1 AND NUCLEAR ACIDS ENCODING SAME, THEIR USES,
 ; AND PROCESSES FOR THEIR PRODUCTION
 ; FILE REFERENCE: P1122
 ; CURRENT APPLICATION NUMBER: US/09/040, 220D
 ; CURRENT FILING DATE: 1998-03-17
 ; NUMBER OF SEQ ID NOS: 8
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-040-220D-2

Query Match 37.2%; Score 742.5; DB 4; Length 345;
 Best Local Similarity 43.6%; Pred. No. 1.8e-68;
 Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYILICANFCSCRDTSATPQSASIKALRNRLRDESNHLTDYRDETQVKGNYV 64
 Db 3 LFGLLLTSLAGQROGTQAESNLSSKFFQSSN--KEQVQD-PQHERITVSTNGSI 58
 QY 65 QSPRFPNSPYRNLLTWRHLIS-QENTRIQVFDNGQFLERENDICRYDVEVEISETS 123
 Db 59 HSPRFHTYPRNTVLYWRLVAVEENWNIQLTDERGLEPDEDICKYDFVEVEPSDGT 118
 QY 124 TIIRGWCGHKEVPRIKSRSNQIKTIFKSDYFVAKPGKLYYSL-LEFPQAPASETN 182
 Db 119 --ILGRWCGSITVPGQKISQNKQIRFVFSDEYFSEPGFCIHYNIUMPOFTEAV---- 171
 QY 183 WESVTSSISGVSYNSVSVTDT-LTADALDKKIAEFTVEDLLK4FNPEQDENMYL 241
 Db 172 -----SISVYSPALRDPDNLNNTAFTSLDRLRLEPERWQDLDLYR 217
 QY 242 DTPRYGRSY-HDRSKR-VDLRDLNDAKRVSCTPRNYSNIREELKLANVVFPRCLV 299
 Db 172 -----SISVYSPALRDPDNLNNTAFTSLDRLRLEPERWQDLDLYR 217
 QY 242 DTPRYGRSY-HDRSKR-VDLRDLNDAKRVSCTPRNYSNIREELKLANVVFPRCLV 299
 ; Sequence 2, Application US/09265686
 ; Patent No. 645283
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
 ; FILE REFERENCE: P1122P2
 ; CURRENT APPLICATION NUMBER: US/09/265, 686
 ; CURRENT FILING DATE: 1999-03-10

RESULT 6
 US-09-457-066-2
 ; Sequence 2, Application US/09457066
 ; Patent No. 6432673
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Shoemaker, Kimberly E.
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: West, James W.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
 ; FILE REFERENCE: 98-60
 ; CURRENT APPLICATION NUMBER: US/09/457, 066
 ; CURRENT FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-457-066-2

Query Match 37.2%; Score 742.5; DB 4; Length 345;
 Best Local Similarity 43.6%; Pred. No. 1.8e-68;
 Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYILICANFCSCRDTSATPQSASIKALRNRLRDESNHLTDYRDETQVKGNYV 64
 Db 3 LFGLLLTSLAGQROGTQAESNLSSKFFQSSN--KEQVQD-PQHERITVSTNGSI 58
 QY 65 QSPRFPNSPYRNLLTWRHLIS-QENTRIQVFDNGQFLERENDICRYDVEVEISETS 123
 Db 59 HSPRFHTYPRNTVLYWRLVAVEENWNIQLTDERGLEPDEDICKYDFVEVEPSDGT 118
 QY 124 TIIRGWCGHKEVPRIKSRSNQIKTIFKSDYFVAKPGKLYYSL-LEFPQAPASETN 182
 Db 119 --ILGRWCGSITVPGQKISQNKQIRFVFSDEYFSEPGFCIHYNIUMPOFTEAV---- 171
 QY 183 WESVTSSISGVSYNSVSVTDT-LTADALDKKIAEFTVEDLLK4FNPEQDENMYL 241
 Db 172 -----SISVYSPALRDPDNLNNTAFTSLDRLRLEPERWQDLDLYR 217
 QY 242 DTPRYGRSY-HDRSKR-VDLRDLNDAKRVSCTPRNYSNIREELKLANVVFPRCLV 299
 Db 218 PTWQOLIGKAFWFGKRSRVNDLNLBEVRLYSCTPRNFSIREELKRTDIFWFGCLL 277
 QY 300 ORCGGNGCGGTIVNWRCTCNSGKTVKHYEVLTQEPGHCIRGRGAKTMAVLDQDHHER 359
 Db 278 KRCGGNCACCLHNCNCQCQCPSKVTKYHEVLQLRP--KTVGVRGLHKSLTDALEHHEE 334
 QY 360 CDCIC 364
 Db 335 CDCVC 339

RESULT 7
 US-09-265-686-2
 ; Sequence 2, Application US/09265686
 ; Patent No. 645283
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
 ; FILE REFERENCE: P1122P2
 ; CURRENT APPLICATION NUMBER: US/09/265, 686
 ; CURRENT FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: US 09/040,220
 PRIOR FILING DATE: 1998-03-17
 PRIOR APPLICATION NUMBER: US 09/184,216
 PRIOR FILING DATE: 1998-11-02
 NUMBER OF SEQ ID NOS: 8
 SEQ ID NO: 2
 LENGTH: 345
 TYPE: PRY
 ORGANISM: Human
 US-09-265-686-2.

Query Match, 37.2%; Score 742.5; DB 4; Length 345;
 Best Local Similarity 43.6%; Pred. No. 1.8e-68; DB 4; Length 345;
 Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYTLICANFCSCRDTSATPOSASTIKLNRNLRDDESNHLIDYRDETOVKGNVY 64
 Db 3 LFGQLLILTSALAGORQGTQAEASNLSSKQFSN--KEQNGVOD-PQHRRITSTNSI 58
 QY 65 QSPRPNSYPRNLITWRLHS-QENTRIOVFDNQGLEAENDICRYDFVEVEDISETS 123
 Db 59 HSPRPHTYPRNTVLUWRLVAEENWVWQIQLTDFERGLPDEDICKYDFVEEPSDGT 118
 QY 124 TIGRWCCHKEVPRIKRTNQIKITFSDDYVAKPGFKIYSL-LEDFQPAASETN 182
 Db 119 --ILGRWCSSGTVPKGQLSKGNQIRFSDPESDFTPEFCIHNIVMQFTEAV--- 171
 QY 183 WESVTTSSIGVSYNSVPTDPT-LIADADKKAEFTDPELDKLYNPNSQEDLENML 241
 Db 172 -----SPSVLPPSALSPLDILNNAATFASTEDDLIRYLERPWQDLEDIKR 217
 QY 242 DTPRVRGRSY-HDRSKV-VDLRUDDAKRYSCTPRNSVNRREELKLANVFPRLCV 299
 Db 218 PTWOLIGKAFVFGKRSRVDLNLTEEVLYSCTPRNSVSRLEKRTDTIWPGCLV 277
 QY 300 QRCGGNCACCLHNCNECOCVPSKVKYHEVLOPFGHKKRRGAKTMAVLVDQLDHHER 359
 Db 278 KRCGGNCACCLHNCNECOCVPSKVKYHEVLOPFGHKKRRGAKTMAVLVDQLDHHER 334
 QY 360 CDCIC 364
 Db 335 CDCIC 339

RESULT 8
 US 09-540-224-5
 Sequence 5. Application US/09540224
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbertson, Debra G.
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; CURRENT APPLICATION NUMBER: US/09/540,224
 ; CURRENT FILING DATE: 2000-03-31
 ; EARLIER APPLICATION NUMBER: US 60/180,169
 ; EARLIER FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 5
 ; LENGTH: 345
 ; TYPE: PRY
 ; ORGANISM: Homo sapiens
 ; US-09-540-224-5

Query Match, 37.2%; Score 742.5; DB 4; Length 345;
 Best Local Similarity 43.6%; Pred. No. 1.8e-68; DB 4; Length 345;
 Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYTLICANFCSCRDTSATPOSASTIKLNRNLRDDESNHLIDYRDETOVKGNVY 64
 Db 3 LFGQLLILTSALAGORQGTQAEASNLSSKQFSN--KEQNGVOD-PQHRRITSTNSI 58
 QY 65 QSPRPNSYPRNLITWRLHS-QENTRIOVFDNQGLEAENDICRYDFVEVEDISETS 123
 Db 59 HSPRPHTYPRNTVLUWRLVAEENWVWQIQLTDFERGLPDEDICKYDFVEEPSDGT 118
 QY 124 TIGRWCCHKEVPRIKRTNQIKITFSDDYVAKPGFKIYSL-LEDFQPAASETN 182
 Db 119 --ILGRWCSSGTVPKGQLSKGNQIRFSDPESDFTPEFCIHNIVMQFTEAV--- 171
 QY 183 WESVTTSSIGVSYNSVPTDPT-LIADADKKAEFTDPELDKLYNPNSQEDLENML 241
 Db 172 -----SPSVLPPSALSPLDILNNAATFASTEDDLIRYLERPWQDLEDIKR 217
 QY 242 DTPRVRGRSY-HDRSKV-VDLRUDDAKRYSCTPRNSVNRREELKLANVFPRLCV 299
 Db 218 PTWOLIGKAFVFGKRSRVDLNLTEEVLYSCTPRNSVSRLEKRTDTIWPGCLV 277
 QY 300 QRCGGNCACCLHNCNECOCVPSKVKYHEVLOPFGHKKRRGAKTMAVLVDQLDHHER 359
 Db 278 KRCGGNCACCLHNCNECOCVPSKVKYHEVLOPFGHKKRRGAKTMAVLVDQLDHHER 334
 QY 360 CDCIC 364
 Db 335 CDCIC 339

RESULT 9
 US-08-572-225-1
 Sequence 1. Application US/08572225
 ; GENERAL INFORMATION:
 ; APPLICANT: Prockop, Darwin J.
 ; APPLICANT: Hojima, Yoshiro
 ; APPLICANT: Li, Shi-Wu
 ; APPLICANT: Siron, Aleksander
 ; APPLICANT: Brenner, Mitch
 ; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Penne & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER: 10036
 ; COMPUTER: IBM PC compatible
 ; COMPUTER: PC-DOS/MS-DOS
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Paintin Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/572,225
 ; FILING DATE: 13-DEC-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8389-031
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-3660
 ; TELEFAX: 415-854-3694
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 788 amino acids.
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-572-225-1

Query Match, 9.4%; Score 187.5; DB 1; Length 788;
 . . .

Best Local Similarity 39.4%; Pred. No. 2e-10; Length 730; Score 186.5; DB 4; Mismatches 43; Conservative 18; Indels 5; Gaps 3; Matches 43; Score 9.4%; Pred. No. 2.3e-10; Length 730; Score 186.5; DB 4; Mismatches 43; Conservative 18; Indels 5; Gaps 3; Matches 43;

Query 59 KGNQYQSPREPNSYPRNLITWRLISQENTRIOLYFDNQGLEEENDICRYDFEYED 118
 Db 399 KLNQSTISPSWPKEPPNKNCTWQLVAPTOYRISQFD--FFETEGNDVCKYDFEVRS 455
 Query 119 ISETSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDFVAKPGFKIY 167
 Db 456 GLTADSKLHGKFCG-SEKPEVITSQYNNNRVEFKSDN-TVSKKGFAHF 502

RESULT 10
 US-08-872-757-2
 ; Sequence 2, Application US/08872757
 ; Patent No. 6258584
 ; GENERAL INFORMATION:
 ; APPLICANT: Prockop, Darwin J.
 ; APPLICANT: Hojima, Yoshio
 ; APPLICANT: Li, Shi-Wu
 ; APPLICANT: Sieron, Aleksander
 ; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/872,757
 ; FILING DATE: 10-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8389-028-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-3660
 ; TELEFAX: 415-854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 730 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-08-872-757-2

Query Match 9.4%; Score 186.5; DB 4; Length 730;
 Best Local Similarity 39.4%; Pred. No. 2.3e-10; Length 730;
 Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

Query 60 KGNQYQSPREPNSYPRNLITWRLISQENTRIOLYFDNQGLEEENDICRYDFEYED 118
 Db 600 KLNQSTISPSWPKEPPNKNCTWQLVAPTOYRISQFD--FFETEGNDVCKYDFEVRS 502
 Query 601 ISETSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDFVAKPGFKIY 167
 Db 602 GLTADSKLHGKFCG-SEKPEVITSQYNNNRVEFKSDN-TVSKKGFAHF 553

RESULT 11
 US-08-872-757-2
 ; Sequence 2, Application US/08872757
 ; Patent No. 6258584
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel E.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Leong, Kalian
 ; APPLICANT: Raiano, Arthur B.
 ; APPLICANT: Saffran, Douglas C.
 ; APPLICANT: Jakobovits, Ayala
 ; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND FILED BY PROSTATE AND BLADDER CANCER CELLS
 ; FILE REFERENCE: 1703-017.US1
 ; CURRENT APPLICATION NUMBER: US/09/374,135
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: 60/095,982
 ; PRIOR FILING DATE: 1998-08-10
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-374-135-6

Query Match 9.1%; Score 180.5; DB 4; Length 101;
 Best Local Similarity 38.7%; Pred. No. 4e-11; Length 101;
 Matches 41; Conservative 18; Mismatches 42; Indels 5; Gaps 3;

Query 62 GYVQSPREPNSYPRNLITWRLISQENTRIOLYFDNQGLEEENDICRYDFEYED 121
 Db 621 GSITSPSWPKEPPNKNCTWQLVAPTOYRISQFD--FFETEGNDVCKYDFEVRSGLT 57
 Query 122 TSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDFVAKPGFKIY 167
 Db 123 58 ADSKKGKFCG-SEKPEVITSQYNNNRVEFKSDN-TVSKKGFAHF 101

RESULT 12
 US-08-872-757-4
 ; Sequence 4, Application US/08872757
 ; Patent No. 6258584
 ; GENERAL INFORMATION:
 ; APPLICANT: Prockop, Darwin J.
 ; APPLICANT: Hojima, Yoshio
 ; APPLICANT: Li, Shi-Wu
 ; APPLICANT: Sieron, Aleksander
 ; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8389-028-999

RESULT 13
 US-09-374-135-6
 ; Sequence 6, Application US/09374135
 ; Patent No. 6277972
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel E.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Leong, Kalian
 ; APPLICANT: Raiano, Arthur B.
 ; APPLICANT: Saffran, Douglas C.
 ; APPLICANT: Jakobovits, Ayala
 ; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND FILED BY PROSTATE AND BLADDER CANCER CELLS
 ; FILE REFERENCE: 1703-017.US1
 ; CURRENT APPLICATION NUMBER: US/09/374,135
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: 60/095,982
 ; PRIOR FILING DATE: 1998-08-10
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-374-135-6

Query Match 9.1%; Score 180.5; DB 4; Length 101;
 Best Local Similarity 38.7%; Pred. No. 4e-11; Length 101;
 Matches 41; Conservative 18; Mismatches 42; Indels 5; Gaps 3;

Query 62 GYVQSPREPNSYPRNLITWRLISQENTRIOLYFDNQGLEEENDICRYDFEYED 121
 Db 621 GSITSPSWPKEPPNKNCTWQLVAPTOYRISQFD--FFETEGNDVCKYDFEVRSGLT 57
 Query 122 TSTIRGRWCGHKEVPPRKSRTNQIKITFKSDDFVAKPGFKIY 167
 Db 123 58 ADSKKGKFCG-SEKPEVITSQYNNNRVEFKSDN-TVSKKGFAHF 101

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 6641 PENNIE

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLogy: linear
MOLECULE TYPE: protein

US-08-872-757-4

Query Match 8.8%; Score 174.5; DB 4; Length 986;
Best Local Similarity 37.6%; Pred No. 6.5e-09;
Matches 41; Conservative 18; Mismatches 45; Indels 5; Gaps 3;

QY 59 KGNQVQSPRPPNSYPRNLLTWRHQSNTROIQLVFDNQFGLEEAENDICRDYFVEED 118
Db 597 KLNQSISSRGCPKEYPPNKNCIWOLVAPQYRISLQFD--FFEEEGNDVCKYDFVEVRS 653

QY 119 ISESTIITGRWCGHKEVPRIKSRNTQKIKITFKSDDYVAKPGFKIY 167
Db 654 GLTADSKLHGKFCG-SEKEPVITSQNNHREVKSDN-TVSKKGKFAHF 700

RESULT 13

US-08-991-408-4
Sequence 4, Application US/08991408
Patient No. 6008017

GENERAL INFORMATION:
APPLICANT: ARLEH, ANTHONY J.

APPLICANT: WILLETT, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.

APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: RATER & PRESTA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA

ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,408
FILING DATE:

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 02-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: PRESTI, PAUL F
REGISTRATION NUMBER: 23-031
REFERENCE/DOCKET NUMBER: ATG-50038

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: protein

US-08-991-408-4

Query Match 8.7%; Score 172.5; DB 3; Length 591;
Best Local Similarity 36.7%; Pred No. 4.6e-09;
Matches 40; Conservative 25; Mismatches 39; Indels 5; Gaps 4;
GENERAL INFORMATION:
PATENT NO. 636515
APPLICANT: ARLEH, ANTHONY J.
APPLICANT: WILLETT, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 60/034,471
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 591
TYPE: PRT
ORGANISM: HOMO SAPIENS

RESULT 14

US-09-432-473-4
Sequence 4, Application US/09432473
Patient No. 636515

GENERAL INFORMATION:

APPLICANT: ARLEH, ANTHONY J.
APPLICANT: WILLETT, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.

TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 60/034,471
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 591
TYPE: PRT
ORGANISM: HOMO SAPIENS

RESULT 15

US-08-866-650-5
Sequence 5, Application US/08866650
Patient No. 593921

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G

TITLE OF INVENTION: Mammalian Tolloid-Like Protein

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US

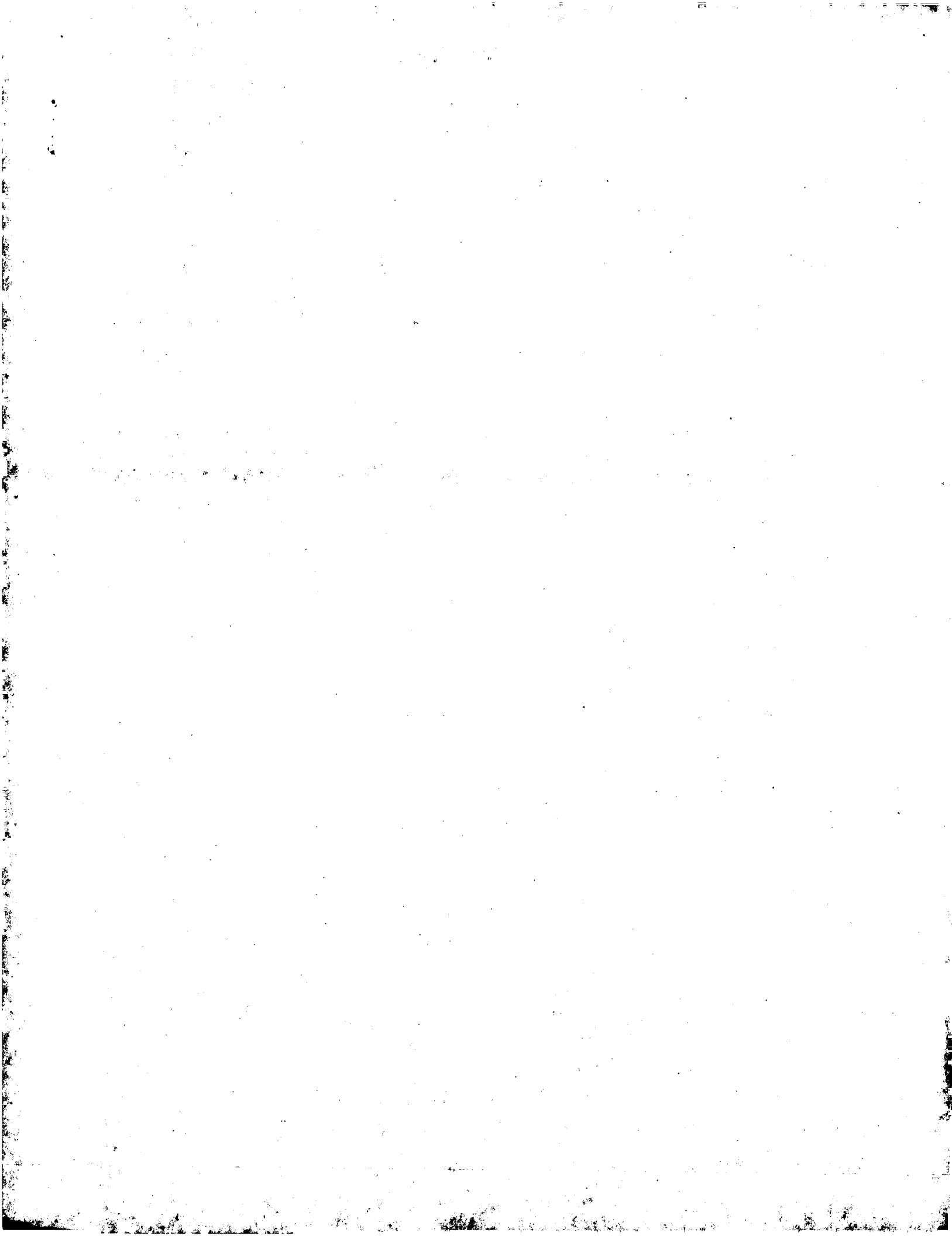
ZIP: 53703
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30



OM protein - protein search, using sw model

Run on: June 12, 2003, 15:32:31 ; Search time 22 Seconds
(without alignments)
1736.314 Million cell updates/sec

Title: US-09-662-783-2

Perfect score: 1944

Sequence: 1 MHLILFVYTLLICANFCSCRD... DIQLDHHERCDCICCSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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9: /cgn2_6/ptodata/2/pubpaas/US09_PUBCOMB_pep:*

10: /cgn2_6/ptodata/2/pubpaas/US10_NEW_PUB_pep:*

11: /cgn2_6/ptodata/2/pubpaas/US10_PUBCOMB_pep:*

12: /cgn2_6/ptodata/2/pubpaas/US10_PUBCOMB_pep:*

13: /cgn2_6/ptodata/2/pubpaas/US60_NEW_PUB_pep:*

14: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1944	100.0	370	9 US-10-086-623-8
2	1944	100.0	370	9 US-10-139-583-37
3	1944	100.0	370	9 US-10-039-474-A2
4	1944	100.0	370	9 US-10-260-539-8
5	1944	100.0	370	9 US-10-264-361-5
6	1944	100.0	370	9 US-10-258-557-5
7	1944	100.0	370	10 US-09-823-033-5
8	1944	100.0	370	10 US-09-808-972-2
9	1944	100.0	370	10 US-09-915-582-56
10	1948	99.7	370	10 US-09-915-582-74
11	1949	97.7	364	9 US-10-028-072-186
12	1949	97.7	364	9 US-10-121-049-186
13	1949	97.7	364	9 US-10-123-904-186
14	1949	97.7	364	9 US-10-147-186
15	1949	97.7	364	9 US-10-175-446-186
16	1949	97.7	364	9 US-10-176-918-186
17	1949	97.7	364	9 US-10-176-921-186
18	1949	97.7	364	9 US-10-137-665-186
19	97.7	364	9	US-10-140-474-186

RESULT 1

US-10-086-623-8

; Sequence 8, Application US/10086623

; Patent No. US2002016470A1

; GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LI, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: UUTELA, Marko

APPLICANT: ALITTAO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES

FILE REFERENCE: 1054/44830C2

CURRENT APPLICATION NUMBER: US/10/086,623

CURRENT FILING DATE: 2000-03-04

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: US 60/157,108

PRIOR FILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: US 60/157,756

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 09/691,200

PRIOR FILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.1

SEQ ID NO 8

SEQUENCE LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

Query Match 100.0%; Score 1994; DB 9; Length 370; Best Local Similarity 100.0%; Pred. No. 3e-61; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 Db 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 QY 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 Db 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 QY 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 Db 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 QY 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 Db 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 QY 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 Db 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 QY 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPR 370
 Db 361 DCICSSRPR 370

RESULT 2
 US-10-139-583-37
 ; Sequence 37, Application US/10139583
 ; Patent No. US2002017193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Shoemaker, Kimberly E.
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: West, James W.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGP3
 ; FILE REFERENCE: 98-60
 ; CURRENT APPLICATION NUMBER: US/10/139, 583
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 09/457, 066
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-039-847A-2

Query Match 100.0%; Score 1994; DB 9; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3e-161; Mismatches 0; Indels 0; Gaps 0;
 Matches 370; Conservative

QY 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 Db 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 QY 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 Db 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 QY 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 Db 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 QY 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 Db 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 QY 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 Db 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 QY 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPR 370
 Db 361 DCICSSRPR 370

RESULT 3
 US-10-039-847A-2
 ; Sequence 2, Application US/10039847A
 ; Publication No. US20020183273A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Topouzis, Stavros
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
 ; TITLE OF INVENTION: KIDNEY FUNCTION
 ; FILE REFERENCE: 00-100
 ; CURRENT APPLICATION NUMBER: US/10/039, 847A
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: US 60/244, 479
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-039-847A-2

Query Match 100.0%; Score 1994; DB 9; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3e-161; Mismatches 0; Indels 0; Gaps 0;
 Matches 370; Conservative

QY 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 Db 1 MHLILFVYLICANFCSCRTSATPOSASIKALRNANLRDESNHLTDIYRRETIQWG 60
 QY 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 Db 61 NGYVQSPRPNSPYRNLITLWRLHSQENTRIQLVFDNOFGLERAEENDICRYDVEVEDIS 120
 QY 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 Db 121 ETSVIRGWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGKIIYSSLEDFOPAASE 180
 QY 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 Db 181 TNWESVTSSISGVSYNSPVTDLIADDKIAEFTVEDILKFNPESQEDLENM 240
 QY 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 Db 241 LDPTRYGRSYHDKSKVLDRLNDADKYSCTPNYSNIREPLKLANVFPRLCIVQ 300
 QY 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGTVNWRSCCTCNSGKTVKYHEVLQFEPGHKRRGRAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPR 370
 Db 361 DCICSSRPR 370

RESULT 4
 US-10-260-539-8

Sequence 8, Application US/10260539
 Publication No. US20030073637A1
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: AASE, Karin
 APPLICANT: Li, Xuri
 APPLICANT: PONTEN, Annica
 APPLICANT: UUTELA, Marko
 APPLICANT: ALITALO, Kari
 APPLICANT: OESTMAN, Arne
 APPLICANT: HELDIN, Carl-Henrik
 TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
 FILE REFERENCE: 1064/44833C2
 CURRENT APPLICATION NUMBER: US/10/260, 539
 CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: US/10/086, 623
 PRIOR FILING DATE: 2000-03-04
 PRIOR APPLICATION NUMBER: US 60/107, 852
 PRIOR FILING DATE: 1998-11-10
 PRIOR APPLICATION NUMBER: US 60/113, 997
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: US 60/150, 604
 PRIOR FILING DATE: 1999-06-26
 PRIOR APPLICATION NUMBER: US 60/157, 108
 PRIOR FILING DATE: 1999-10-04
 PRIOR APPLICATION NUMBER: US 60/157, 756
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 09/438, 046
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: US 09/691, 200
 PRIOR FILING DATE: 2000-10-19
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 8
 LENGTH: 370
 TYPE: PRT
 ORGANISM: Homo sapiens
 ;
 ; US-10-260-539-8
 ;
 Query Match 100.0%; Score 1994; DB 9; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3e-161;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MHLRLIVYTICANFSCCRDNTSATOSASTKALRNANRDRDESNHITDLYRDETTQVKG 60
 Db 1 MHLRLIVYTICANFSCCRDNTSATOSASTKALRNANRDRDESNHITDLYRDETTQVKG 60
 Qy 61 NGYVQSPRFPSYPRNLLWRLHSOENTRQLVFDNQGLEEANDICRYDFVVEDIS 120
 Db 61 NGYVQSPRFPSYPRNLLWRLHSOENTRQLVFDNQGLEEANDICRYDFVVEDIS 120
 Qy 121 ETSTIRGRWCGHKEVPRIKSRTNQIKIFKSDIDFVAKGFKIYISLLEDQPARASE 180
 Db 121 ETSTIRGRWCGHKEVPRIKSRTNQIKIFKSDIDFVAKGFKIYISLLEDQPARASE 180
 Qy 181 TNWESTTSISGVSYNSPSVNDPTIADALKKIARFDTVDLKYFNPSQEDLENMY 240
 Db 181 TNWESTTSISGVSYNSPSVNDPTIADALKKIARFDTVDLKYFNPSQEDLENMY 240
 Qy 241 LDTPRGRGSYHDKSKVUDLNDAKRSCPTPRIVSYNIREELKANVFPROLLVQ 300
 Db 241 LDTPRGRGSYHDKSKVUDLNDAKRSCPTPRIVSYNIREELKANVFPROLLVQ 300
 Qy 301 RCGGNGCGTGNWRSCTCNSGKTVKHYEVIFQEPCHIKRGRAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGTGNWRSCTCNSGKTVKHYEVIFQEPCHIKRGRAKTMALVDIQLDHERC 360
 Qy 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370
 RESULT 6
 US-10-258-557-2
 Sequence 2, Application US/10258557
 Publication No. US20030100502A1
 GENERAL INFORMATION:
 APPLICANT: Beals, John
 APPLICANT: Gonzalez-Bewhitt, Patricia
 APPLICANT: Hammond, Lissa
 APPLICANT: Lu, Jirong
 APPLICANT: Na, Songqing
 APPLICANT: Su, Eric
 APPLICANT: Witcher, Derrick
 TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF
 FILE REFERENCE: X-14392M
 CURRENT APPLICATION NUMBER: US/10/258, 557
 CURRENT FILING DATE: 2002-10-23
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 2
 LENGTH: 370
 TYPE: PRT

ORGANISM: Homo sapiens
US-10-258-557-2

Query Match 100.0%; Score 1994; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 3e-161; Gaps 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Db 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Qy 61 NGYVQSPREPNSYPRNLLTWRLHSQENTRIQLOVFDNQGLEAENDICRYDVEVEDIS 120
61 NGYVQSPREPNSYPRNLLTWRLHSQENTRIQLOVFDNQGLEAENDICRYDVEVEDIS 120

Db 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180
121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180

Qy 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180
121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180

Db 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180
121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180

Qy 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240
Db 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240

Qy 241 LDTPRYRGSYHDKSKVLDLDRDAKKYSCPRNYSNIREELKLANVFFPRLVQ 300
Db 241 LDTPRYRGSYHDKSKVLDLDRDAKKYSCPRNYSNIREELKLANVFFPRLVQ 300

Qy 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360
Db 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360

Qy 361 DCTCSSRPR 370
Db 361 DCTCSSRPR 370

RESULT 7
US-09-823-033-5
; Sequence 5, Application US/09823033
; -PATENT NO. US2002004425AI
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gibertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-19
; CURRENT APPLICATION NUMBER: US 09/808, 972
; CURRENT FILING DATE: 2001-03-14
; PRIORITY NUMBER: US 60/235, 295
; PRIORITY NUMBER: US 60/164, 463
; PRIORITY NUMBER: US 60/132, 250
; PRIORITY NUMBER: US 60/180, 169
; PRIORITY NUMBER: US 60/235, 295
; PRIORITY NUMBER: US 60/164, 463
; PRIORITY FILING DATE: 1999-11-10
; PRIORITY FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; -US-09-808-972-2

Query Match 100.0%; Score 1994; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 3e-161; Gaps 0; Indels 0; Gaps 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Db 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Qy 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180
Db 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180

Qy 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240
Db 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240

Qy 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360
Db 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360

Qy 361 DCTCSSRPR 370
Db 361 DCTCSSRPR 370

RESULT 8
US-09-808-972-2
; Sequence 2, Application US/09808972
; PATENT NO. US2002006482AI
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gibertson, Debra G.
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-19
; CURRENT APPLICATION NUMBER: US 09/808, 972
; CURRENT FILING DATE: 2001-03-14
; PRIORITY NUMBER: US 60/235, 295
; PRIORITY NUMBER: US 60/164, 463
; PRIORITY NUMBER: US 60/132, 250
; PRIORITY NUMBER: US 60/180, 169
; PRIORITY NUMBER: US 60/235, 295
; PRIORITY NUMBER: US 60/164, 463
; PRIORITY FILING DATE: 1999-11-10
; PRIORITY FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; -US-09-808-972-2

Query Match 100.0%; Score 1994; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 3e-161; Gaps 0; Indels 0; Gaps 0;

Qy 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Db 1 MHLILFVYTILICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLYRDETQKG 60
Qy 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180
Db 121 ETSPIRGRWCGKEVPRIKSRNQIKITFKSDYFVAKPGKIVYSLDEDQPAASE 180

Qy 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240
Db 181 TNWESVTSSISGVSYNSPSPVTDPTLADALDKKIAEFDVTDLKYFNPESWQEDLENM 240

Qy 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360
Db 301 RCGGNCGCGTVNWRSCTCNSGKTVKYHEVLQFEGHIKRRGAKTMALVDIQLDHERC 360

Qy 361 DCTCSSRPR 370
Db 361 DCTCSSRPR 370

FILE REFERENCE: PS723P1
 CURRENT APPLICATION NUMBER: US/09/915, 582
 PRIOR APPLICATION NUMBER: 2001-07-27
 PRIOR APPLICATION NUMBER: PCT/US01/01431
 PRIOR APPLICATION NUMBER: 2001-01-17
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/180, 628
 PRIOR APPLICATION NUMBER: 60/231, 968
 PRIOR FILING DATE: 2000-09-12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 74
 LENGTH: 370
 TYPE: PR
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (216)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-09-915-582-74
 Query Match 99.7%; Score 1988; DB 10; Length 370;
 Best Local Similarity 100.0%; Score 1994; DB 10; Length 370;
 Matches 370; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MHLRLFVYTILCANFCSRCRTSATPOSASIKALRNLNRDDESNLTDYRDETIQVKG 60
 Db 1 MHLRLFVYTILCANFCSRCRTSATPOSASIKALRNLNRDDESNLTDYRDETIQVKG 60
 QY 61 NGYVOSPRFPNSYPRNLITWRLHSQENTRQLVFDNQGLEEENDICRYDFVEEDIS 120
 Db 61 NGYVOSPRFPNSYPRNLITWRLHSQENTRQLVFDNQGLEEENDICRYDFVEEDIS 120
 QY 121 ETSTTIRGRMGHKEVPRKSRTRNQIKITFKSDYFVAAPGFKIYSLLEDFOAASE 180
 Db 121 ETSTTIRGRMGHKEVPRKSRTRNQIKITFKSDYFVAAPGFKIYSLLEDFOAASE 180
 QY 181 TNWESTTSSISGVSYNSPVSYDPTLADAKKIAEFTDVEDLKYFNPSPQEDLENMY 240
 Db 181 TNWESTTSSISGVSYNSPVSYDPTLADAKKIAEFTDVEDLKYFNPSPQEDLENMY 240
 QY 241 LDTPRYRGSYHDKRSKVDLDRNDAKRTSCTPRNVSNTREELKLANVFPCLLIVQ 300
 Db 241 LDTPRYRGSYHDKRSKVDLDRNDAKRTSCTPRNVSNTREELKLANVFPCLLIVQ 300
 QY 301 RCGGNGCGGTYNWRSCTCNSGKTVKYHEVLQFEPGHIKRRGAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGGTYNWRSCTCNSGKTVKYHEVLQFEPGHIKRRGAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370
 RESULT 10
 US-09-915-582-74
 ; Sequence 74, Application US/0915582
 ; Patent No. US2002120103A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 17 Human Secreted Proteins

RESULT 9
 US-09-915-582-56
 ; Sequence 56, Application US/0915582
 ; Patent No. US2002120103A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 17 Human Secreted Proteins

Query Match 99.7%; Score 1988; DB 10; Length 370;
 Best Local Similarity 100.0%; Score 1994; DB 10; Length 370;
 Matches 370; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MHLRLFVYTILCANFCSRCRTSATPOSASIKALRNLNRDDESNLTDYRDETIQVKG 60
 Db 1 MHLRLFVYTILCANFCSRCRTSATPOSASIKALRNLNRDDESNLTDYRDETIQVKG 60
 QY 61 NGYVOSPRFPNSYPRNLITWRLHSQENTRQLVFDNQGLEEENDICRYDFVEEDIS 120
 Db 61 NGYVOSPRFPNSYPRNLITWRLHSQENTRQLVFDNQGLEEENDICRYDFVEEDIS 120
 QY 121 ETSTTIRGRMGHKEVPRKSRTRNQIKITFKSDYFVAAPGFKIYSLLEDFOAASE 180
 Db 121 ETSTTIRGRMGHKEVPRKSRTRNQIKITFKSDYFVAAPGFKIYSLLEDFOAASE 180
 QY 181 TNWESTTSSISGVSYNSPVSYDPTLADAKKIAEFTDVEDLKYFNPSPQEDLENMY 240
 Db 181 TNWESTTSSISGVSYNSPVSYDPTLADAKKIAEFTDVEDLKYFNPSPQEDLENMY 240
 QY 241 LDTPRYRGSYHDKRSKVDLDRNDAKRTSCTPRNVSNTREELKLANVFPCLLIVQ 300
 Db 241 LDTPRYRGSYHDKRSKVDLDRNDAKRTSCTPRNVSNTREELKLANVFPCLLIVQ 300
 QY 301 RCGGNGCGGTYNWRSCTCNSGKTVKYHEVLQFEPGHIKRRGAKTMALVDIQLDHERC 360
 Db 301 RCGGNGCGGTYNWRSCTCNSGKTVKYHEVLQFEPGHIKRRGAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370
 RESULT 11
 US-10-028-072-186
 ; Sequence 186, Application US/10028072
 ; Publication No. US200300431A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filovoroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanae, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang
 TITLE OF INVENTION:
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/028,072
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
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 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
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 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/064809
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 PRIOR FILING DATE: 1997-11-17
 PRIOR APPLICATION NUMBER: 60/066364
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 PRIOR FILING DATE: 1997-11-24
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 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/069334
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069694
 PRIOR FILING DATE: 1997-12-16
 PRIOR APPLICATION NUMBER: 60/072320
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/073612
 PRIOR FILING DATE: 1998-02-04
 PRIOR APPLICATION NUMBER: 60/074086
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 60/074092
 PRIOR FILING DATE: 1998-01-23
 PRIOR APPLICATION NUMBER: 60/07791
 PRIOR FILING DATE: 1998-02-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/079710
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081695
 PRIOR FILING DATE: 1998-04-14
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081818
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082999
 PRIOR FILING DATE: 1998-04-24
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085149
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086414

PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086430
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088730
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088741
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089949
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090538
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07

Query Match 97.7%; Score 1949; DB 9; Length 364;
 Best Local Similarity 98.4%; Pred. No. 1.9e-157; Mismatches 0; Indels 6; Gaps 1;
 Matches 364; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MRLILFVYTLCIANFCSCRDTSATPOSASIKALRNANLRDESNHITDLYRDETIQVKG 60
 Db 1 MRLILFVYTLCIANFCSCRDTSATPOSASIKALRNANLRD-----DLYRDETIQVKG 54
 QY 61 NGYVQSPRPNPSYPRNLLTWRLHSQENTRQLVFDNQFGLEEAENDICRDYFVEEDIS 120
 Db 55 NGYVQSPRPNPSYPRNLLTWRLHSQENTRQLVFDNQFGLEEAENDICRDYFVEEDIS 114
 QY 121 ETSTIRGRWCQHKEPPIRKTSRNTQKIKTFRSDDYFVAKPGFKIYSSLEDFOPAASE 180
 Db 115 ETSTIRGRWCQHKEPPIRKTSRNTQKIKTFSDYFVAKPGFKIYSSLEDFOPAASE 174
 QY 181 TNWEVTSISGSVSYNSPSVTDPITLADALDKKIAERDTVEDLLKIFNPESQEDLENM 240
 Db 175 TNWEVTSISGSVSYNSPSVTDPITLADALDKKIAERDTVEDLLKIFNPESQEDLENM 234
 Db 115 ETSTIRGRWCQHKEPPIRKTSRNTQKIKTFSDYFVAKPGFKIYSSLEDFOPAASE 174
 QY 241 LDPTRYGRSYHDKSKVLDLDDAKRYSCTPRNYSVNTREELKLANVFPCLIVQ 300
 Db 235 LDPTRYGRSYHDKSKVLDLDDAKRYSCTPRNYSVNTREELKLANVFPCLIVQ 294
 QY 301 RGGNCGCGTVMWRSCCNSGKTVKKHEVLOFEGHIKRRGRAKTMALVDIOLDHERC 360
 Db 295 RGGNCGCGTVMWRSCCNSGKTVKKHEVLOFEGHIKRRGRAKTMALVDIOLDHERC 354
 QY 361 DCICSSRPR 370
 Db 355 DCICSSRPR 364

RESULT 12
 US-10-121-049-186
 ; Sequence 186, Application US/10121049
 ; Publication No. US20030022239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Trumans, Daniel
 ; APPLICANT: Wattabre, Colin K
 ; APPLICANT: Zhang, Zemin
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330RC17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; PRIOR Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO: 186
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-121-049-186

Query Match 97.7%; Score 1949; DB 9; Length 364;
 Best Local Similarity 98.4%; Pred. No. 1.9e-157; Mismatches 0; Indels 6; Gaps 1;
 Matches 364; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MRLILFVYTLCIANFCSCRDTSATPOSASIKALRNANLRDESNHITDLYRDETIQVKG 60
 Db 1 MRLILFVYTLCIANFCSCRDTSATPOSASIKALRNANLRD-----DLYRDETIQVKG 54
 QY 61 NGYVQSPRPNPSYPRNLLTWRLHSQENTRQLVFDNQFGLEEAENDICRDYFVEEDIS 120
 Db 55 NGYVQSPRPNPSYPRNLLTWRLHSQENTRQLVFDNQFGLEEAENDICRDYFVEEDIS 114
 QY 121 ETSTIRGRWCQHKEPPIRKTSRNTQKIKTFSDYFVAKPGFKIYSSLEDFOPAASE 180
 Db 115 ETSTIRGRWCQHKEPPIRKTSRNTQKIKTFSDYFVAKPGFKIYSSLEDFOPAASE 174
 QY 181 TNWEVTSISGSVSYNSPSVTDPITLADALDKKIAERDTVEDLLKIFNPESQEDLENM 240
 Db 175 TNWEVTSISGSVSYNSPSVTDPITLADALDKKIAERDTVEDLLKIFNPESQEDLENM 234
 QY 241 LDPTRYGRSYHDKSKVLDLDDAKRYSCTPRNYSVNTREELKLANVFPCLIVQ 300
 Db 295 RGGNCGCGTVMWRSCCNSGKTVKKHEVLOFEGHIKRRGRAKTMALVDIOLDHERC 354
 QY 301 RGGNCGCGTVMWRSCCNSGKTVKKHEVLOFEGHIKRRGRAKTMALVDIOLDHERC 360
 Db 355 DCICSSRPR 364

RESULT 13
 US-10-123-904-186
 ; Sequence 186, Application US/10123904
 ; Publication No. US20030022328A1
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watnabe, Colin K.
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C54

CURRENT APPLICATION NUMBER: US/10/1123, 904

CURRENT FILING DATE: 2002-04-16

Prior Application removed - See file Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 186
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-123-904-186

Query Match 97.7%; Score 1949; DB 9; Length 364;
 Best Local Similarity 98.4%; Pred. No. 1.9e-157;
 Matches 364; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MHLRLFVYTLLICANPCSCRTSATPOSASIKALRNANLRDESNHLTDYRDETTQKG 60
 1 MHLRLFVYTLLICANPCSCRTSATPOSASIKALRNANLRDESNHLTDYRDETTQKG 54
 1 MHLRLFVYTLLICANPCSCRTSATPOSASIKALRNANLRDESNHLTDYRDETTQKG 54

QY 61 NGYYVOSPRPPNSPYRNLLTWRHLSQENTRQLYFDNQGLEEENDICRYDVEVELIS 120
 55 NGYYVOSPRPPNSPYRNLLTWRHLSQENTRQLYFDNQGLEEENDICRYDVEVELIS 114

Db 175 TNWESVTSSISGVSYNSPVTDPLIADALKKAEFDTVEDLKYFNESESQEDLENM 240
 175 TNWESVTSSISGVSYNSPVTDPLIADALKKAEFDTVEDLKYFNESESQEDLENM 234

QY 181 TNWESVTSSISGVSYNSPVTDPLIADALKKAEFDTVEDLKYFNESESQEDPAASE 180
 181 TNWESVTSSISGVSYNSPVTDPLIADALKKAEFDTVEDLKYFNESESQEDPAASE 174

Db 241 LDTPRYRGSYHDKSKVLDLNDAKRYSCTPRNYSVNRKELKLAVVFPCLLWQ 300
 241 LDTPRYRGSYHDKSKVLDLNDAKRYSCTPRNYSVNRKELKLAVVFPCLLWQ 294

QY 301 RCGGNCCGCTVNRSTCNSKGTVKYHEVLOFEPGHIKRRGAKTMAVLVDIOLDHHERC 360
 295 RCGGNCCGCTVNRSTCNSKGTVKYHEVLOFEPGHIKRRGAKTMAVLVDIOLDHHERC 354

Db 361 DCICSSRPR 370
 361 DCICSSRPR 370

Db 355 DCICSSRPR 364
 355 DCICSSRPR 364

RESULT 14
 US-10-140-470-186
 Sequence 186, Application US/10140470
 Publication No. US20030022331A1

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RESULT 15
 US-10-175-746-186
 Sequence 186, Application US/10175746
 Publication No. US20030027270A1

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